



PCT09

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,954A

DATE: 03/13/2003

TIME: 13:38:21

Input Set : A:\EP.txt

Output Set: N:\CRF4\03132003\I830954A.raw

3 <110> APPLICANT: SOLOMON, Beka
 4 FRENKEL, Dan
 5 HANAN, Eilat
 7 <120> TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN
 DIAGNOSING
 8 AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
 10 <130> FILE REFERENCE: SOLOMON=2C
 12 <140> CURRENT APPLICATION NUMBER: 09/830,954A
 13 <141> CURRENT FILING DATE: 2001-05-03
 15 <150> PRIOR APPLICATION NUMBER: PCT/IL00/00518
 16 <151> PRIOR FILING DATE: 2000-08-31
 18 <150> PRIOR APPLICATION NUMBER: 09/629,971
 19 <151> PRIOR FILING DATE: 2000-07-31
 21 <150> PRIOR APPLICATION NUMBER: US 09/473,653
 22 <151> PRIOR FILING DATE: 1999-12-29
 24 <150> PRIOR APPLICATION NUMBER: US 60/152,417
 25 <151> PRIOR FILING DATE: 1999-09-03
 27 <160> NUMBER OF SEQ ID NOS: 29
 29 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 4
 33 <212> TYPE: PRT
 34 <213> ORGANISM: Artificial
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Synthetic peptide
 39 <400> SEQUENCE: 1
 41 Glu Phe Arg His
 42 1
 45 <210> SEQ ID NO: 2
 46 <211> LENGTH: 15
 47 <212> TYPE: PRT
 48 <213> ORGANISM: Artificial
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Synthetic peptide
 53 <400> SEQUENCE: 2
 55 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 56 1 5 10 15
 59 <210> SEQ ID NO: 3
 60 <211> LENGTH: 43
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Artificial
 64 <220> FEATURE:
 65 <223> OTHER INFORMATION: Synthetic peptide
 67 <400> SEQUENCE: 3

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69 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
 70 1 5 10 15
 73 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
 74 20 25 30
 77 Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
 78 35 40

81 <210> SEQ ID NO: 4

82 <211> LENGTH: 4

83 <212> TYPE: PRT

84 <213> ORGANISM: Artificial

86 <220> FEATURE:

87 <223> OTHER INFORMATION: Synthetic peptide

89 <400> SEQUENCE: 4

91 Trp Val Leu Asp

92 1

95 <210> SEQ ID NO: 5

96 <211> LENGTH: 717

97 <212> TYPE: DNA

98 <213> ORGANISM: Homo sapiens

100 <220> FEATURE:

101 <221> NAME/KEY: CDS

102 <222> LOCATION: (1)..(717)

103 <223> OTHER INFORMATION:

W--> 105 <400> 5

106 cag gtc aaa ctg cag gag tca ggg gct gag ctg gtg agg cct ggg gtc 48
 107 Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
 108 1 5 10 15
 110 tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gat tat 96
 111 Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 112 20 25 30
 114 gct atg cac tgg gtg aag cag agt cat gca aag agt cta gag tgg att 144
 115 Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
 116 35 40 45
 118 gga gtt att agt act tac tat ggt gat gct agc tac aac cag aag ttc 192
 119 Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
 120 50 55 60
 122 aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat 240
 123 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 124 65 70 75 80
 126 atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt 288
 127 Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
 128 85 90 95
 130 gca aga ggg gct act atg tcc tac ttt gac tac tgg ggc caa gtg acc 336
 131 Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
 132 100 105 110
 134 acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga gtt ggc tct 384
 135 Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser
 136 115 120 125
 138 ggc ggt ggc gga tcg gac atc gag ctc act cag tct cca gca atc atg 432

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139 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
140      130      135      140
142 tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca      480
143 Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
144 145      150      155      160
146 agt ata agt tac atg cac tgg tat cag cag aag cca ggc acc tcc ccc      528
147 Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro
148      165      170      175
150 aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct      576
151 Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
152      180      185      190
154 cgc ttc agt ggc agt ggg tct ggg acc tct tat tct ctc aca atc agc      624
155 Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
156      195      200      205
158 agc atg gag gct gaa gat gct gcc act tat tac tgc cat cag cgg agt      672
159 Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
160      210      215      220
162 agt tac cca ttc acg ttc gga ggg ggg gcc aag ctg gaa ata aaa      717
163 Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
164 225      230      235
167 <210> SEQ ID NO: 6
168 <211> LENGTH: 239
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <400> SEQUENCE: 6
174 Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val
175 1      5      10      15
178 Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
179      20      25      30
182 Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
183      35      40      45
186 Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
187      50      55      60
190 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
191 65      70      75      80
194 Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
195      85      90      95
198 Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
199      100      105      110
202 Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Val Gly Ser
203      115      120      125
206 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
207      130      135      140
210 Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
211 145      150      155      160
214 Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro
215      165      170      175
218 Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
219      180      185      190

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222 Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 223 195 200 205
 226 Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
 227 210 215 220
 230 Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
 231 225 230 235

234 <210> SEQ ID NO: 7

235 <211> LENGTH: 6

236 <212> TYPE: PRT

237 <213> ORGANISM: Artificial

239 <220> FEATURE:

240 <223> OTHER INFORMATION: Synthetic peptide

242 <400> SEQUENCE: 7

244 Tyr Tyr Glu Phe Arg His

245 1 5

248 <210> SEQ ID NO: 8

249 <211> LENGTH: 15

250 <212> TYPE: PRT

251 <213> ORGANISM: Artificial

253 <220> FEATURE:

254 <223> OTHER INFORMATION: Synthetic peptide

256 <400> SEQUENCE: 8

258 Val His Glu Pro His Glu Phe Arg His Val Ala Leu Asn Pro Val

259 1 5 10 15

262 <210> SEQ ID NO: 9

263 <211> LENGTH: 3

264 <212> TYPE: PRT

265 <213> ORGANISM: Artificial

267 <220> FEATURE:

268 <223> OTHER INFORMATION: Synthetic peptide

270 <400> SEQUENCE: 9

272 Lys Leu His

273 1

276 <210> SEQ ID NO: 10

277 <211> LENGTH: 45

278 <212> TYPE: DNA

279 <213> ORGANISM: Artificial

281 <220> FEATURE:

282 <223> OTHER INFORMATION: Primer

284 <220> FEATURE:

285 <221> NAME/KEY: misc_feature

286 <222> LOCATION: (17)..(17)

287 <223> OTHER INFORMATION: n is A, C, T or G

290 <400> SEQUENCE: 10

W--> 291 ccccccctccg aacgtsnatg ggtaactcga tcgctgatgg cagta

294 <210> SEQ ID NO: 11

295 <211> LENGTH: 24

296 <212> TYPE: DNA

297 <213> ORGANISM: Artificial

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```

299 <220> FEATURE:
300 <223> OTHER INFORMATION: Primer
302 <400> SEQUENCE: 11
303 atctatgcgg ccagccggc catg
306 <210> SEQ ID NO: 12
307 <211> LENGTH: 38
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Primer
314 <400> SEQUENCE: 12
315 gtggtgctga gtggatccta tactacactg ccaccggg
318 <210> SEQ ID NO: 13
319 <211> LENGTH: 58
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Primer
326 <400> SEQUENCE: 13
327 agctccgatg ctgaattcgg tgatagcggc tacgaagtgc atcatcagaa acctgcag
330 <210> SEQ ID NO: 14
331 <211> LENGTH: 52
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Primer
338 <400> SEQUENCE: 14
339 ggtttctgat gatgcacttc gtagccgcta tcatgacgaa attcagcatc gg
342 <210> SEQ ID NO: 15
343 <211> LENGTH: 9
344 <212> TYPE: PRT
345 <213> ORGANISM: Artificial
347 <220> FEATURE:
348 <223> OTHER INFORMATION: Synthetic peptide
350 <400> SEQUENCE: 15
352 His Gln Arg Ser Ser Tyr Pro Cys Thr
353 1 5
356 <210> SEQ ID NO: 16
357 <211> LENGTH: 9
358 <212> TYPE: PRT
359 <213> ORGANISM: Artificial
361 <220> FEATURE:
362 <223> OTHER INFORMATION: Synthetic peptide
364 <400> SEQUENCE: 16
366 His Gln Arg Ser Ser Tyr Pro Cys Thr
367 1 5
370 <210> SEQ ID NO: 17
371 <211> LENGTH: 9
372 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/830,954A

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Input Set : A:\EP.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 17

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

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L:105 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:103
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:527 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:525